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EXAMINER	
THOMAS, DAVID C	
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1637	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/529,319	DRANCOURT ET AL.	
	Examiner	Art Unit	
	DAVID C. THOMAS	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *12 September 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-4,6-12,15-18,20 and 21* is/are pending in the application.

4a) Of the above claim(s) *15-18 and 20* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4,6-12 and 21* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. The previous Office Action is withdrawn and replaced by this supplemental Office Action. This is in response to the traversal that claims 6-12 and 21 should have been examined in the previous Office Action since these claims were included in the originally elected Group I, as was discussed in a phone interview with Applicant's agent on February 20, 2008. The Examiner agrees that claims 6-12 and 21 were improperly withdrawn, and thus claims 1-4, 6-12 and 21 of Group I will now be examined on the merits. Claims 15-18 and 20 were previously withdrawn.

The previous requirement for restriction of invention groups, as discussed in the first previous Office Action, is still deemed proper and the restriction is therefore made FINAL.

Claim Interpretation

2. Prior to examination of the claims, the claims must first be construed.

Applicants defined the term "complementary sequences" as follows (see page 17 of the specification, lines 14-19):

"In the present description, by "reverse sequences and complementary sequences" is meant the following sequences: the reverse sequence of said sequence, the complementary sequence of said sequence, and the complementary sequence of the reverse sequence of said sequence". Therefore, with regard to the term "complementary sequences", any sequence that comprises ad few as one complementary base is considered complementary to a given nucleic acid sequence since there is no strict definition of the term "complementary sequences".

Applicants exemplify the term "oligonucleotide" in the following way (page 7, lines 19-21): "A nucleotide fragment (or oligonucleotide) may for example contain up to 100 nucleotide motifs". However, this is not a definition of the term and therefore, isolated oligonucleotides or mixtures of oligonucleotides as cited in the claims are anticipated by oligonucleotides of any length.

Claim Rejections - 35 USC § 112

3. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 1-4, 6-12 and 21 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Part (b) of claims 1-3 is drawn to an isolated rpoB gene or gene fragment comprising a nucleic acid sequence complementary to the elected SEQ ID NOS: 1 or 8, specific to the bacterium genus *Streptococcus*. Similarly, part (c) of claims 1-4 is drawn to an isolated rpoB gene or gene fragment comprising a nucleic acid sequence having 98.7% homology to the elected SEQ ID NOS: 1 or 8 or sequences complementary to SEQ ID NOS: 1 or 8. The instant specification only describes the nucleic acids comprising SEQ ID NOS: 1 and 8. Applicants did not adequately describe a representative number of sequences complementary to SEQ ID NOS: 1 or 8 or those

having 98.7% homology to the elected SEQ ID NOS: 1 or 8 or complementary sequences. With regard to claim 4, Applicants did not adequately describe a representative number of oligonucleotide sequences complementary to sequences having at least 20 consecutive nucleotides of SEQ ID NO: 8 or those having 98.7% homology to sequences having at least 20 consecutive nucleotides of the elected SEQ ID NO: 8 or complementary sequences. In fact, only one sequence was provided, that of SEQ ID NO: 8.

For example, a polynucleotide comprising a sequence with 98.7% sequence identity to SEQ ID NO: 1 would contain 4462 bp identical to SEQ ID NO: 1. If the polynucleotide was 4523 bp long, it would have 59 bp different from SEQ ID NO: 1. Considering that each of the 59 bp can be one of four bases, the number of sequences of 4523 bp 98.7% identical to SEQ ID NO: 1 would be 4^{59} or about 3.3×10^{35} sequences. Since there is no limit on the length of such polynucleotides, the number of such molecules is in the order of billions of billions. Similarly, a polynucleotide comprising a sequence with 98.7% sequence identity to SEQ ID NO: 8 would contain 700 bp identical to SEQ ID NO: 8. If the polynucleotide was 709 bp long, it would have 9 bp different from SEQ ID NO: 8. Considering that each of the 9 bp can be one of four bases, the number of sequences of 709 bp 98.7% identical to SEQ ID NO: 8 would be 4^9 or about 2.6×10^5 sequences. Since there is no limit on the length of such polynucleotides, the number of such molecules is also in the order of billions.

With regard to claims 6-12 and 21, Applicants did not adequately describe a representative number of oligonucleotide sequences comprising a sequence including

at least 8 consecutive nucleotides of SEQ ID NOS: 6 or 7 or sequences complementary to sequences comprising a sequence including at least 8 consecutive nucleotides of SEQ ID NOS: 6 or 7. In fact, only two sequences were provided, that of SEQ ID NOS: 6 and 7, comprising degenerate bases or inosine at selected positions.

In analysis of the claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note regarding genus/species situations that "Satisfactory disclosure of a ``representative number'' depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: Federal Register: December 21, 1999 (Volume 64, Number 244), revised guidelines for written description.)

All of the current claims encompass a genus of nucleic acids which are different from those disclosed in the specification. With regard to claims 1-4, the genus includes nucleic acid variants for which no written description is provided in the specification, since sequences either need only to have one complementary base to SEQ ID NOS: 1 or 8 or have at least 98.7% homology to SEQ ID NOS: 1 or 8 or complementary sequences, but could also contain additional completely unrelated sequences of unlimited length. This large genus is represented in the specification by only the particularly named SEQ ID NO: 1 with 4,523 bp and SEQ ID NO: 8 with 709 bp. With regard to claims 6-12 and 21, the genus also includes nucleic acid variants for which no written description is provided in the specification, since sequences either need only to

have 8 consecutive nucleotides of SEQ ID NOS: 6 or 7 or complementary sequences, but could also contain additional completely unrelated sequences comprised in the oligonucleotides, which may be up to 100 bp in total length. This large genus is represented in the specification by only the particularly named SEQ ID NO: 6 with 20 nucleotides and SEQ ID NO: 7 with 23 nucleotides. Thus, applicant has express possession of only four particular sequences, in a genus which comprises billions of different possibilities.

It is noted in the recently decided case The Regents of the University of California v. Eli Lilly and Co. 43 USPQ2d 1398 (Fed. Cir. 1997) decision by the CAFC that

> "A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. See Fiers, 984 F.2d at 1169- 71, 25 USPQ2d at 1605- 06 (discussing Amgen). It is only a definition of a useful result rather than a definition of what achieves that result. Many such genes may achieve that result. The description requirement of the patent statute requires a description of an invention, not an indication of a result that one might achieve if one made that invention. See In re Wilder, 736 F.2d 1516, 1521, 222 USPQ 369, 372- 73 (Fed. Cir. 1984) (affirming rejection because the specification does "little more than outlin[e] goals appellants hope the claimed invention achieves and the problems the invention will hopefully ameliorate."). Accordingly, naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material. "

In the current situation, the definition of the nucleic acid sequences from claims 1-4 (b) and (c) and claims 6-12 and 21 lack any specific structure, and is precisely the situation of naming a type of material which is generally known to likely exist, but, except for the four specific sequences, is in the absence of knowledge of the material composition and fails to provide descriptive support for the claims.

In the instant application, certain specific SEQ ID NOS are described. Also, in Vas-Cath Inc. v. Mahurkar (19 USPQ2d 1111, CAFC 1991), it was concluded that:

> "...applicant must also convey, with reasonable clarity to those skilled in art, that applicant, as of filing date sought, was in possession of invention, with invention being, for purposes of "written description" inquiry, whatever is presently claimed."

In the application at the time of filing, there is no record or description which would demonstrate conception of any nucleic acids other than those expressly disclosed which comprise SEQ ID NOS: 1 and 6-8. Therefore, the claims fail to meet the written description requirement by encompassing sequences which are not described in the specification.

Claim Rejections - 35 USC § 102

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

6. Claims 1, 3, 4, 6 and 21 are rejected under 35 U.S.C. 102(b) as being anticipated by Haselbeck et al. (U.S. Patent Pub. No. 2002/0061569).

With regard to claims 1 and 3, Haselbeck teaches an isolated *rpoB* gene fragment of the genus *Streptococcus* comprising:

(b) complementary sequences of an isolated rpoB gene or gene fragment comprising SEQ ID NO: 8 (positions 2278-2309 of SEQ ID NO: 9089 taught by

Haselbeck representing sequences of *Streptococcus pneumoniae* are 100% homologous to positions 1-32 of SEQ ID NO: 8, a span of 32 consecutive nucleotides; in addition, positions 2548-2603 of SEQ ID NO: 9089 are 100% homologous to positions 271-326 of SEQ ID NO: 8, a span of 56 consecutive nucleotides; note: there are no arbitrary bases in SEQ ID NO: 8).

With regard to claim 4, Haselbeck teaches an isolated oligonucleotide comprising:

(a) a nucleic acid sequence specific to a bacterium of the genus *Streptococcus,* and comprising 20-100 consecutive nucleotides included in SEQ ID NO: 8 (positions 2278-2309 of SEQ ID NO: 9089 taught by Haselbeck representing sequences of *Streptococcus pneumoniae* are 100% homologous to positions 1-32 of SEQ ID NO: 8, a span of 32 consecutive nucleotides; in addition, positions 2548-2603 of SEQ ID NO: 9089 are 100% homologous to positions 271-326 of SEQ ID NO: 8, a span of 56 consecutive nucleotides).

With regard to claim 6, Haselbeck teaches an isolated oligonucleotide comprising a sequence of at least of at least 12 nucleotides, including at least one sequence of 8 consecutive nucleotides included in one of the following sequences:

SEQ ID NO: 6: 5'- AARYTNGGMCCTGAAGAAAT-3', and

SEQ ID NO: 7: 5'- TGNARTTTRTCATCAACCATGTG-3' in which:

N represents inosine or one of the 4 nucleotides A, T, C or G,

R represents A or G,

M represents A or C, and

Y represents C or T,

and complementary sequences thereof (positions 44-25 of SEQ ID NO: 992 taught by Haselbeck is homologous to all 20 nucleotides of SEQ ID NO: 6 when R represents A, Y represents T, N represents A and M represents A).

With regard to claim 21, Haselbeck teaches an oligonucleotide as defined in claim 6 wherein the sequence has 18-35 nucleotides (positions 44-25 of SEQ ID NO: 992 taught by Haselbeck is homologous to a sequence of 20 nucleotides of SEQ ID NO: 6 when R represents A, Y represents T, N represents A and M represents A).

7. Claims 1-4, 6 and 21 are rejected under 35 U.S.C. 102(b) as being anticipated by Kunsch et al. (U.S. Patent No. 6,420,135).

With regard to claims 1 and 3, Kunsch teaches an isolated *rpoB* gene fragment of the genus *Streptococcus* comprising:

(b) complementary sequences of an isolated rpoB gene or gene fragment comprising SEQ ID NO: 8 (positions 11613-11582 of SEQ ID NO: 111 taught by Kunsch representing sequences of *Streptococcus pneumoniae* are 100% homologous to positions 1-32 of SEQ ID NO: 8, a span of 32 consecutive nucleotides; in addition, positions 11343-11288 of SEQ ID NO: 111 are 100% homologous to positions 271-326 of SEQ ID NO: 8, a span of 56 consecutive nucleotides; note: there are no ambiguous bases in SEQ ID NO: 8).

With regard to claim 2, Kunsch teaches an isolated *rpoB* gene fragment of the genus *Streptococcus* comprising:

(b) complementary sequences of an isolated rpoB gene or gene fragment comprising SEQ ID NO: 1 (positions 10692-10658 of SEQ ID NO: 111 taught by Kunsch representing sequences of *Streptococcus pneumoniae* are 100% homologous to positions 3531-3565 of SEQ ID NO: 8, a span of 35 consecutive nucleotides; in addition, positions 10395-10367 of SEQ ID NO: 111 are 100% homologous to positions 3789-3817 of SEQ ID NO: 1, a span of 29 consecutive nucleotides).

With regard to claim 4, Kunsch teaches an isolated oligonucleotide comprising:

(a) a nucleic acid sequence specific to a bacterium of the genus *Streptococcus,* and comprising 20-100 consecutive nucleotides included in SEQ ID NO: 8 (positions 11613-11582 of SEQ ID NO: 111 taught by Kunsch representing sequences of *Streptococcus pneumoniae* are 100% homologous to positions 1-32 of SEQ ID NO: 8, a span of 32 consecutive nucleotides; in addition, positions 11343-11288 of SEQ ID NO: 111 are 100% homologous to positions 271-326 of SEQ ID NO: 8, a span of 56 consecutive nucleotides).

With regard to claim 6, Kunsch teaches an isolated oligonucleotide comprising a sequence of at least of at least 12 nucleotides, including at least one sequence of 8 consecutive nucleotides included in one of the following sequences:

SEQ ID NO: 6: 5'- AARYTNGGMCCTGAAGAAAT-3', and

SEQ ID NO: 7: 5'- TGNARTTTRTCATCAACCATGTG-3' in which:

N represents inosine or one of the 4 nucleotides A, T, C or G,

R represents A or G,

M represents A or C, and

Y represents C or T,

and complementary sequences thereof (positions 10898-10920 of SEQ ID NO: 111 taught by Kunsch is homologous to all 23 nucleotides of SEQ ID NO: 7 when N represents C and R represents A).

With regard to claim 21, Kunsch teaches an oligonucleotide as defined in claim 6 wherein the sequence has 18-35 nucleotides (positions 10898-10920 of SEQ ID NO: 111 taught by Kunsch is homologous to a sequence of 23 nucleotides of SEQ ID NO: 7 when N represents C and R represents A).

Conclusion

8. Claims 1-4, 6-12 and 21 are rejected. No claims are allowable. However, with regard to claims 7-12, no prior art was found that teaches equimolar mixtures of oligonucleotides as defined in claim 6, with each having a different sequence.

Correspondence

9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to David C. Thomas whose telephone number is 571-272-3320 and whose fax number is 571-273-3320. The examiner can normally be reached on 5 days, 9-5:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

David C. Thomas
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March 13, 2008